IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of: Li et al.

Application No: 09/348,815   Art Unit: 1635

Filed: July 8, 1999   Examiner: Zara, J.

For: **Connective Tissue Growth Factor-2**   Attorney Docket No: PF126P1D1

<u>**Declaration Of Donna Dimke Under 37 C.F.R. § 1.132**</u>

Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

     I, Donna Dimke, hereby declare and state as follows:

    1.   I am employed by Human Genome Sciences, Inc. (HGS), Rockville,

Maryland, as Group Leader of Gene Discovery. Since I began working at HGS in March of

1993, my duties have primarily included carrying out and analyzing, as both a bench scientist

and a manager, extensive DNA sequencing.

    2.   A partially redacted copy of the American Type Culture Collection (ATCC)

deposit receipt for deposit number 75804 is attached hereto as Exhibit A. As the deposit

receipt indicates, ATCC deposit number 75804 contains a DNA plasmid assigned the HGS

Code Number 242,847, also known within HGS as HGS Clone ID HLFBE49XX. Exhibit B

is a partially redacted Sequence Worksheet printout from the HGS electronic notebook for

HGS Code Number 242,847, which shows the nucleotide sequence of HGS Code Number

242,847 and the correlation between this code number and HGS Clone ID HLFBE49XX. I

requested from the ATCC a sample of ATCC deposit 75804 by a purchase order numbered

70038 dated May 15, 2000 (a partially redacted copy of which is attached hereto as Exhibit

C). I received the sample of ATCC deposit 75804 from the ATCC in June of 2000, as

evidenced by Sales Order # SO171485 from the ATCC (a partially redacted copy of which is attached hereto as Exhibit D).

3.   I determined the nucleotide sequence of the cDNA clone contained in the sample of the ATCC deposit number 75804 that I received from the ATCC in June of 2000. I have been shown what has been presented to me as Figures 1A-C as originally filed in U.S. Application No. 08/459,101 (hereinafter "original Figures 1A-C"), a copy of which original Figures 1A-C is attached hereto as Exhibit E. I used the nucleotide sequence of HGS Code 242,847, the coding portion of which is shown in original Figures 1A-C, as a reference to determine the nucleotide sequence of the cDNA clone contained in the plasmid of ATCC deposit number 75804. A sample of ATCC deposit number 75804 was thoroughly sequenced under my supervision in my laboratory at HGS. More specifically, a single plasmid isolate obtained from the sample of ATCC deposit number 75804 was initially identified by obtaining sequence information from near the 5'-end of the clone. Then, 20-mer primers were designed based on the HGS Code 242,847 nucleotide sequence to obtain sequence information covering the clone two to nine times over. The sequencing was carried out on an Applied Biosystems, Inc. (ABI) 377 automated sequencer using the ABI dye terminator kit, according to the manufacturer's instructions. The data obtained from this sequence analysis is summarized in Exhibit F, attached hereto, which shows an alignment of the individual sequencing runs performed on the sample of ATCC deposit number 75804 I received, as well as the sequence originally assigned to Clone ID HLFBE49XX (*i.e.*, HGS Code 242,847).

4.   The correct nucleotide and encoded amino acid sequence for the cDNA clone contained in ATCC Deposit Number 75804 is shown in the corrected version of Figures 1A-C attached hereto as Exhibit G. Exhibit H is a marked up version of original Figures 1A-C showing in red ink the differences between the nucleotide and amino acid sequence in the

original figures and the correct nucleotide and encoded amino acid sequence of the cDNA

clone of ATCC Deposit Number 75804 of Exhibit G.

5.   Based on the experiments described above and the high degree of similarity

between the nucleotide and amino acid sequences of original Figures 1A-C and the correct

corresponding sequences as shown in Exhibit H, it is my belief that a person of ordinary skill

in the art, upon routine sequencing of the cDNA of clone contained in ATCC deposit number

75804 using methods well known in the art prior to July 12, 1994, would readily determine

that the correct sequence of the cDNA clone is the sequence shown in Exhibit G, especially

when using original Figures 1A-C as a guide.

6.   I hereby declare that all statements made herein of my own knowledge are true

and that all statements made on information and belief are believed to be true; and further that

these statements were made with the knowledge that willful false statements and the like so

made are punishable by fine or imprisonment, or both, under § 1001 of Title 18 of the United

States Code, and that such willful false statements may jeopardize the validity of the

application captioned above or any patent issuing thereupon.

Date: ___10/17/00___   _Donna Dimke_

                                                        Donna Dimke

American *Type* Culture Collection

12301 Parklawn Drive • Rockville, MD 20852 USA • Telephone: (301)231-5520 Telex: 898-055 ATCCNORTH • FAX: 301-770-2587

BUDAPEST TREATY ON THE INTERNATIONAL RECOGNITION OF
THE DEPOSIT OF MICROORGANISMS FOR THE PURPOSES OF PATENT PROCEDURE

INTERNATIONAL FORM

RECEIPT IN THE CASE OF AN ORIGINAL DEPOSIT ISSUED PURSUANT TO RULE 7.3
AND VIABILITY STATEMENT ISSUED PURSUANT TO RULE 10.2

To: (Name and Address of Depositor or Attorney)

Human Genome Sciences, Inc.
Attention: Craig A. Rosen, Ph.D.
9620 Medical Center Drive, Suite 300
Rockville, MD 20850

Deposited on Behalf of: Human Genome Sciences, Inc.

Identification Reference by Depositor: ATCC Designation

DNA Plasmid, 242,847   75804

The deposits were accompanied by: __ a scientific description __ a proposed taxonomic description indicated above.

The deposits were received June 7, 1994 by this International Depository Authority and have been accepted.

AT YOUR REQUEST:

__X__   We will inform you of requests for the strains for 30 years.

The strains will be made available if a patent office signatory to the Budapest Treaty certifies one's right to receive, or if a U.S. Patent is issued citing the strains.

If the cultures should die or be destroyed during the effective term of the deposit, it shall be your responsibility to replace them with living cultures of the same.

The strains will be maintained for a period of at least 30 years after the date of deposit, and for a period of at least five years after the most recent request for a sample. The United States and many other countries are signatory to the Budapest Treaty.

The viability of the cultures cited above was tested June 14, 1994. On that date, the cultures were viable.

International Depository Authority: American Type Culture Collection, Rockville, Md. 20852 USA

Signature of person having authority to represent ATCC:
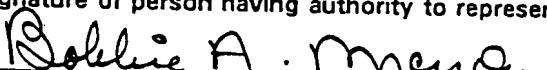
_____ Date: June 20, 1994
Bobbie A. Brandon, Head, ATCC Patent Depository

cc: Greg Ferraro

Human Genome Sciences, Inc.
Sequence Worksheet
HLFBE49XX:

Sequence Information

Gene Name: Homo sapiens mRNA for hCYR61 protein.

HGS Code: 242847

Sequence ID: **HLFBE49XX**

Search Results

Sequence

```
>HLFBE49XX
GGCACAGAGCC CGCCCCGCGCC AGCCCTTGCC TCCCTGCCCA CCGCGCCACC GCGCCGCCACC
CCGACCCCGC TGCGACGGGC TGTCCGGCTGC ACACCAGCTT GTTGGTGTCT TCGTTCGGCGC
GCTCGCCCCG GGTTACTCCT GCGCGACACA ATGAGCTCCC GAATGTTCAG GGAGCTCGCC
TTAGTTCGTCA CCCTTCTCTCA CTTGACCAGG GTGGGGCTCT CCACCTTGCCC CGCTGACTGC
CACTGCCCCC TGGAGCGGCC CAAGTCGCGCG CCCGGAGTCG GGCTGGTTCGG GGACGGCTTGC
GGCTGTTGTA AGGTCTCGGCC CAAGCAGCTC AACGAGGACT GCAGAAAAAC GCAGCCCTGC
GACCACACCA AGGGGCTGGA ATGCCAACTTC GCGCCCAGCT CCACCGCTCT GAAGGGATC
TGCAGAGCTC AGTCAGAGGG CAGACCCCGT GAATATAACT CCAGAATCTA CCAAAACGGG
GAAAGTTTCC AGCCCAACTG TAAACATCAG TGCACATGTA TTGGATGCCG CCGGGGGGCT
TGCATTCCTC TGTGTCCCCA AGAACTATCT CTCCCCAACT TGGGCTGTCC CAACCCTCGG
CTGGTCAAAG TTACGGGCA GTCCTCGGAG GAGTGGGTCT GTGAGCGAGGA TAGTATCAAG
GACCCCATGG AGGACCAGGA CGGCCTCCTT GGCAAGGGGC TGGGATTCGA TGCCTCCGGAG
GTGGAGTTGA CCGAGAAACAA TGAATTGATT GCAGTTGGAA AAGGCAGCTC ACTGAAGGGG
CTCCCTGTTT TTTGAATGGA GCCTCGCATC CTATACAAAC CTTTACAAGG CCAGAAATGT
ATTGTTCAAA CAACTTCATG GTCCCAGTGC TCAAAGACCT GTGGAACTGG TATCTCCACA
CCGAGTTACCA ATGACAAACC TGAGTGCCGC CTTGTGAAAG AAACCGGAT TTGTGAGTG
CGGCCTTGTG GACAGCGCAGT GTACAGCAGC CTGAAAAAG GCAAGAAATG CAGCCAGACC
AAGAAAATCCC CCGAACCAGT CAGGTTTACT TACGCTGGAT GTTTGAGTGT GAAGAAATAC
CGGCCCCAAGT ACTGCGGTTC CTGGCGTGGAC GGCCGATGCT GCACGCCCCA GCTGACCAGG
ACTGTGTAAGA TGCGGTTCCC CTGCGAAGAT GGGGAAGACAT TTTCCAAGAA CGTCATGATG
ATCCAGTTCCT CCAAATGCAA CTACAACTGC CCGCATGCCA ATGAAGCAGC GTTTCCCTTC
```

REDACTE

Human Genome Sciences, Inc.

Sequence Worksheet

HGS HLFBE49XX:

```
TACAGGCTGT TCCAATGACA TTCACAAATT TAGGGACTAA ATGCTACCTG GGTTTCCAGG
GCACACCTAG ACCAAACAAG GGAGAAGAGT GTCAGAATCA GAATCATGGA GAAAATGGGC
GGGGGTGGTG TGGGTGATGG GACTCATTGT AGAAAGGAAG CCTTGCTTCAT TCTTGAGGAG
CATTAAGGTA TTTCGAAACT CCCAAGGGTG CTGGTGCGGA TGGACACTAA TGCAGCCACG
ATTTGGAGAAT ACTTTGCTTC ATAGTATTGG ACCACATGTT ACTGCTTTCAT TTTTGGAGCTT
GTGGAGTTGA TGACTTTCTG TTTTCTGTTT GTAAATTATT TGCTAAGCCAT ATTTTCTCTA
GGCTTTTTTC CTTTTGGGGT TCTTACAGTCG TAAAAGAGAT AATAAAGATTA GTTGGACAGT
TTAAAGCTTT TATTTGTTCT TTGACAAAAG TAAATGGGAG GGCCATTCCAT CCCTTCCTGG
AGGGGACAC TCCATGAGTG TCTGTTGAGAG GCAGCTATCT GCACTCTAAA CTGCAAACAG
AAATTCAGGTG TTTTAAGACT GAATGTTTTA TTTATTCAAAA TGTTAGCTTTT GGGGAGGGAG
GCGAAAATGTA ATACTTGGAAT AATTTGTAAA TGATTTTTAAT TTTATTATTCA GTGAAAAGAT
TTTATTTATG GAATTAACCA TTTTAATTAAAG AAATATTTTAC CTAAAAAAAA AAAAAAAAAA
AAA*
```

Sequence Notes

HGS

Human Genome Sciences, Inc.
9410 Key West Avenue, Rockville, MD 20850
(301) 309-8504   (301) 738-0290 fax
Federal ID # 22-3178468   Tax Exempt # 06505640

Purchase Order # _70038_

BILL AND SHIP TO ABOVE ADDRESS   Vendor Ref. # _SO171485_

Requisitioner to complete in clear, legible text	
Date request filled out: 5/15/00	
Requisitioner: Donna Dimble Ext.: 2147	
Building: 9480 Floor: 1st Lab: G DISC.	
Suggested vendor: ATCC	
Use this vendor only: ☒ Yes	
Date needed: 5/24/00	

PART #	QTY	*U/M	DESCRIPTION	PAGE	USER: UNIT $	TOTAL $			STATUS
	1		1 vial ATCC deposit # 75804		Free $0	50			
	1		vial ATCC deposit		Free	$0 00			
	1		vial ATCC deposit		Free	$0 00			
					TOTAL	$0 00			

ACCT CODES		EXTRA CHARGES	SIGNATURES	
LINE #	DEPT. #: 165	ACCT. #: 6010	Shipping/Handling $24.50	Requisitioner/Date: Donna Dimble 5/1
			Dry Ice	Approved by/Date:
			Freight	Approved by/Date:
	PROJECT ACCT. #:		Misc.	Approved by/Date:
	TAXABLE? ☐ YES ☐ NO			

* Suggest examples – cs, ea, units, pk, g, ml., IL

WHITE COPY – Purchasing   YELLOW COPY – Administration   PINK COPY – Requisitioner's Confirmation   GOLD COPY – Requisitioner's Original

rev. 8/99

REDACTED

ATCC™

PACKING LIST

10801 University Boulevard
Manassas, Virginia, 20110-2209 USA
703-365-2700 FAX: 703-365-2750
EMAIL: sales@atcc.org

ATCC 10801 University Blvd. Manassas, VA 20110-2209 USA
EMERGENCY RESPONSE: Chemtrec (800) 424-9300 or (202) 483-7616

SHIP-TO:

SALES ORDER #: SO171485

BILL-TO:

29219
Human Genome Sciences Inc
Accounts Payable
9410 Key West Ave
Rockville, MD 20850

10014301
Human Genome Sciences Inc
9410 Key West Ave
Rockville, MD 20850
USA

ATTN:
TEL #: 301-309-8504   FAX#: 301-309-8512

ATTN: Dimke, Donna
TEL #: 301-610-5790   FAX#: 301-279-0175

CUSTOMER P.O. #: 70038

SOLD TO:	29219	FOB: Manassas, VA	SHIPPED VIA: Alert	FREIGHT LIST
ORDER DATE:	06/05/00			
SALESPERSON:	nhiggins	BOL:	SHIP DATE: 06/12/00	FZ-NON

#	B S L	ITEM NUMBER	U M	QTY SHIP	QTY B.O.	DESCRIPTION	PRICE	NET PRICE
001	1	75804 ~~HEPAH75~~ HLFBE49XX	EA	1	0	RESTRICTED PATENT, REFER ALL ORDERS	0.00	0.00
002	1		EA	1	0	RESTRICTED PATENT, REFER ALL ORDERS	0.00	0.00
003	1		EA	1	0	RESTRICTED PATENT, REFER ALL ORDERS	.0.00	0.00

Taxable Total: 0.00
Tax[1]: 05.00%   Tax[2]: 00.00%   Tax[3]: 00.00%
Amount Pre-Paid: 0.00

Line Total: 0.00
Total Tax: 0.00

Shipping & Handling: 24.50

? Discount: 0.00
USD Grand Total: 24.50

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FIG. IA

```
ATGAGCTCCCGAATCGTCAGGGAGCTCGCCTTAGTCGTGTTCCTTCCACTTGACCAGG
 M   S   S   R   I   V   R   E   L   A   L   V   V   L   L   H   L   T   R

GTGGGGCTCTCCACCTGCCCCGCTGACTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG
 V   G   L   S   T   C   P   A   D   C   H   C   P   L   E   A   P   K   C   A

CCGGGAGTCGGGGCTGGTTCCGGGACGGGCTGCGGCTGCTGTTTGTAAGGTCTGCGCCAAGCAGCTC
 P   G   V   G   L   V   R   D   G   C   G   C   C   K   V   C   A   K   Q   L

AACGAGGACTGCAGAAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC
 N   E   D   C   R   K   T   Q   P   C   D   H   T   K   G   L   E   C   N   F

GGCGGCCAGCTCCACCGCCTCTGAAGGGGGGATCTGCAGAGCTCAGTCAGAGGGGAGACCCTGT
 G   A   S   T   A   L   K   G   I   C   R   A   Q   S   E   G   R   P   C

GAATATAACTCCAGAATCTACCAAAACGGGGGAAAGTTTCCAGCCAACTGTAAACATCAG
 E   Y   N   S   R   I   Y   Q   N   G   E   S   F   Q   P   N   C   K   H   Q

TGCACATGTATTGGATGGCGCGGGGGGGCTTGCATTCCTCTGTGTCCCCAGAACTATCT
 C   T   C   I   G   W   R   G   A   C   I   P   L   C   P   Q   E   L   S

CTCCCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACGGGCAGTGCTGCGAG
 L   P   N   L   G   C   P   N   P   R   L   V   K   V   T   G   Q   C   C   E
```

MATCH WITH FIG. IB

FIG. IB

```
GAGTGGGGTCTTGTTGACGAGGAGGATAGTAGTATCAAGGACCCCATGGAGGACCAGGACGGGCCTCCTT
E    W    V    C    D    E    D    S    I    K    D    P    M    E    D    Q    D    G    L    L

GGCAAGGGGGCTGGGGATTCGATGCCTCCGAGGGTGGAGTTGACGAGAAACAATGAATTGATT
G    K    G    L    G    F    D    A    S    E    V    E    L    T    R    N    N    E    L    I

GCAGTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCCTGTTTTTGGAATGGAGCCTCGCATC
A    V    G    K    G    S    S    L    K    R    L    P    V    F    G    M    E    P    R    I

CTATACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGC
L    Y    N    P    L    Q    G    Q    K    C    I    V    Q    T    T    S    V    S    Q    C

TCAAAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGC
S    K    T    C    G    T    G    I    S    T    R    V    T    N    D    N    P    E    C    R

CTTGTGTGAAAGAAACCCGGATTTGTTGAGGTGCGGGCTTGTGTGGACAGCCAGTGTACAGCAGC
L    V    K    E    T    R    I    C    E    V    R    P    C    G    Q    P    V    Y    S    S

CTGAAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCGAACCAGTCAGGTTTACT
L    K    K    G    K    K    C    S    K    T    K    K    S    P    E    P    V    R    F    T
```

FIG. IC

```
TACGCTGGATGTTTGAGTGTGAAGAAATACCGGCCAAGTACTGCGGTTCCTGCGTGGAC
 Y  A  G  C  L  S  V  K  K  Y  R  P  K  Y  C  G  S  C  V  D

GGCCGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGAGATGCGGTTCCCCTGCGAAGAT
 G  R  C  C  T  P  Q  L  T  R  T  V  K  M  R  F  P  C  E  D

GGGGAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTCCAAATGCAACTACAACTGC
 G  E  T  F  S  K  N  V  M  M  I  Q  S  S  K  C  N  Y  N  C

CCGCATGCCAATGAAGCAGCCGTTTCCCTTCTACAGGCTGTGTTCCAATGA
 P  H  A  N  E  A  A  F  F  Y  R  L  F  Q  *
```

FIG. 2A

```
  1 MSSRIVRELALVVTLLHLTRVGLSTCPADCHCPLEAPKCAPGVGLVRDGC  50
    |||...|..|.:.||:.|||||||||| .||||||||||||||||||||||
  1 MSSSTFRTLAVAVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGC  50

 51 GCCKVCAKQLNEDCRKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPC 100
    |||||||||||||| .|||||||||||||||||||||||||||||||||||
 51 GCCKVCAKQLNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPC 100

101 EYNSRIYQNGESFQPNCKHQCTCIGWRRGACIPLCPQELSLPNLGCPNPR 150
```

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FIG. 2B

```
101 EYNSRIYQNGESFQPNCKHQCTCID.GAVGCIPLCPQELSLPNLGCPNPR 149
    |||||||||||||||||||||||||.:|||||||||||||||||||||||
151 LVKVTGQCCEEWVCDEDSIKDPMEDQDGLLGKGLGFDASEVELTRNNELI 200

150 LVKVSGQCCEEWVCDEDSIKDSLDDQDDL....LGLDASEVELTRNNELI 195
    ||||.:||||||||||||||||.::|||:|    |:||||||||||||||
151 LVKVTGQCCEEWVCDEDSIKDPMEDQDGLLGKGLGFDASEVELTRNNELI 200

201 AVGKGSSLKRLPVFGMEPRILYNPL...QGQKCIVQTTSWSQCSKTCGTGI 248
    |:|||||||||||||||.||:||:|    ||||||||||||||||.|||||
196 AIGKGSSLKRLPVFGTEPRVLFNPLHAHGQKCIVQTTSWSQCSKSCGTGI 245

249 STRVTNDNPECRLVKETRICEVRPCGQPVYSSLKRKGKKCSKTKKSPEPVR 298
    ||||||||||||||||||||||||||||||||||||.||||||||||||||
246 STRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKKCSKTKKSPEPVR 295

299 FTYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFPCEDGETFSKNV 348
    ||||||.|||||||||||||||||||||.|||||||||.||||||.||||
296 FTYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNV 345

349 MMIQSSKCNYNCPHANEAAFPFYRLFQ 375
    ||||:||||||||||:||.:|:|.:|.|
346 MMIQSCKCNYNCPHPNEASFRLYSLFN 372
```

FIG. 3

```
  1 MSSRIVRELALVVTLLHL.TRVGLS.TCPADCHCPLE.APKCAPGVGLVR  47
    | . .:: .|:.| ||.| :|:.|| .|.|.:| :|.|:||
  1 MLASVAGPISLALVLLALCTRPATGQDCSAQCQCAAEAAPHCPAGVSLVL  50

 48 DGGGCCKVCAKQLNEDCRKTQPCDHTKGLECNFGASSTALKGICRAQSEG  97
    |||||||||:||| .|:.|.:| ||| |||:| .:||.||
 51 DGGCCRVCAKQLGELCTERDPCDPHKGLFCDFGSPANRKIGVCTAK.DG   99

 98 RPCEYNSRIYQNGESFQPNCKHQCTCIGWRRGACIPLCPQELSLPNLGCP 147
    ||.| :||||:: .:|:.||| |:.|| .::||.| :||
100 APCVFGGSVYRSGESFQSSCKYQCTCLD.GAVGCVPLCSMDVRLPSPDCP 148

148 NPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLGKGLGFDASEVELTRNN 197
    :|: ||.|||||||||| .:| :: |:|| :|
149 FPRRVKLPGKCCKEWVCDEPKDRTAV.........GPALAAYRLEDT...: 186

198 ELIAVGKGSSLKRLPVFGMEPRILYNPLQGQKCIVQTTSWSQCSKTCGTG 247
                  .: |.:|| .||.||||||||||.|||||.|
187 ...........FGPDPTMM......RANCLVQTTEWSACSKTCGMG      215

248 ISTRVTNDNPECRLVKETRICEVRPCGQPVVYSSLKKGKKCSKTKKSPEPV 297
    ||||||||| :.||.| .:.||.|| ||||||||.| :||
216 ISTRVTNDNTFCRLEKQSRLCMVRPCEADLEENIKKGKKCIRTPKIAKPV  265

298 RFTYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFPCEDGETFSKN 347
    :.|:.|| ||.|.|| .|.||||||||.:.|:..:| ||.|.:|.||
266 KFELSGCTSVKTYRAKFCGVCTDGRCCTPHRTTTLPVEFKCPDGEIMKKN 315

348 VMMIQSSKCNYNCPHANE..AAFPFYRLFQ 375
    :|:|. :|||||||| .| .| : :: ::
316 MMFIKTCACHYNCPGDNDIFESLYRKMYG  345
```

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HLFBEXXF1A   GGCACGAGCCCGCCCGCCGCCCAGCCCTCGCCTCCCTGCCCACCGGGCCCACCGCGCCGCC
HLFBEXXRA   GGCACGAGCCCGCCCGCCGCCCAGCCCTCGCCTCCCTGCCCACCGGGCCCACCGCGCCGCC
HLFBEXXR   GGCACGAGCCCGCCCGCCGCCCAGCCCTCGCCTCCCTGCCCACCGGGCCCACCGCGCCGCC
HLFBE49XX   GGCACGAGCCCGCCCGC:GCC:AGCCCTCGCCTCCCTGCCCACCGG:CCCACCGCGCCGC:
        #1   _____

              GGCACGAGCCCGCCCGCCGCCCAGCCCTCGCCTCCCTGCCCACCGGGCCCACCGCGCCGCC
                                    .   .   .   .

HLFBEXXF1A   ACCCCGACCCCGCTGCGCANGGCCTGTCCGCTGCACACCAGCTTGTTGGCGTCTTCGTCGC
HLFBEXXRA   ACCCCGACCCCGCTGCGCACGGCCTGTCCGCTGCACACCAGCTTGTTGGCGTCTTCGTCGC
HLFBEXXR   ACCCCGACCCCGCTGCGCACGGCCTGTCCGCTGCACACCAGCTTGTTGGCGTCTTCGTCGC
HLFBE49XX   ACCCCGACCCCGCTGCG:ACGGGCTGTCCGCTGCACACCAGCTTGTTGGTGTCTTCGTCGG
       #62   _____

              ACCCCGACCCCGCTGCGCACGGCCTGTCCGCTGCACACCAGCTTGTTGGCGTCTTCGTCGC
                            . + .   .   .

HLFBEXXF1A   CGCGCTCGCCCCGGGCTACTCCTGCGCGCCNCAATGAGCT
HLFBEXXRA   CGCGCTCGCCCCGGGCTACTCCTGCGCGCCACAATGAGCTCCCGCATCGCCAGGGCGCTCG
HLFBEXXR   CGCGCTCGCCCCGGGCTACTCCTGCGCGCCACAATGAGCTCCCGCATCGCCAGGGCGCTCG
HLFBE49XX   CGCGCTCGCCCCGGGTTACTCCTGCGCGACACAATGAGCTCCCGAATCGTCAGGGAGCTCG
HLFBEXXR1   CGCCACAATGAGCTCCCGCATCGCCAGGGCGCTCG
      #123   _____

              CGCGCTCGCCCCGGGCTACTCCTGCGCGCCACAATGAGCTCCCGCATCGCCAGGGCGCTCG
                                    .   +   .   .   .

HLFBEXXRA   CCTTAGTCGTCACCCTTCTCCACTTGACCAGGCTGGCGCTCTCCACCTGCCCCGCTGCCTG
HLFBEXXR   CCTTAGTCGTCACCCTTCTCCACTTGACCAGGCTGGCGCTCTCCACCTGCCCCGCTGCCTG
HLFBE49XX   CCTTAGTCGTCACCCTTCTCCACTTGACCAGGGTGGGGCTCTCCACCTGCCCCGCTGACTG
HLFBEXXR1   CCTTAGTCGTCACCCTTCTCCACTTGACCAGGCTGGCGCTCTCCACCTGCCCCGCTGCCTG
      #184   _____

              CCTTAGTCGTCACCCTTCTCCACTTGACCAGGCTGGCGCTCTCCACCTGCCCCGCTGCCTG
                                    .   .   .

HLFBEXXRA   CCACTGCCCCCTGGAGGCGCCCAAGTGCGCGCCGGGAGTCGGGCTGGTCCGGGACGGCTGC
HLFBEXXR   CCACTGCCCCCTGGAGGCGCCCAAGTGCGCGCCGGGAGTCGGGCTGGTCCGGGACGGCTGC
HLFBE49XX   CCACTGCCCCCTGGAGGCGCCCAAGTGCGCGCCGGGAGTCGGGCTGGTCCGGGACGGCTGC
HLFBEXXR1   CCACTGCCCCC
      #245   _____

              CCACTGCCCCCTGGAGGCGCCCAAGTGCGCGCCGGGAGTCGGGCTGGTCCGGGACGGCTGC

HLFBEXXRA   GGCTGCTGTAAGGTCTGCGCCAAGCAGCTCAACGAGGACTGCAGCAAAACGCAGCCCTGCG
HLFBEXXR   GGCTGCTGTAAGGTCTGCGCCAAGCAGCTCAACGAGGACTGCAGCAAAACGCAGCCCTGCG
HLFBE49XX   GGCTGTTGTAAGGTCTGCGCCAAGCAGCTCAACGAGGACTGCAGAAAAACGCAGCCCTGCG
HLFBE49R   TCTGCGCCAAGCAGCTCAACGAGGACTGCAGCAAAACGCAGCCCTGCG
HLFBEXXR2A   GCAAAACGCAGCCCTGCG
      #306   _____

              GGCTGCTGTAAGGTCTGCGCCAAGCAGCTCAACGAGGACTGCAGCAAAACGCAGCCCTGCG
                    .   .

HL.FBEXXRA   ACCACACCAAGGGGCTGGAATGCAACTTCGGCGCCAGCTCCACCGCTCTGAAGGGGATCTG
HL.FBEXXR   ACCACACCAAGGGGCTGGAATGCAACTTCGGCGCCAGCTCCACCGCTCTGAAGGGGATCTG
HL.FBE49XX   ACCACACCAAGGGGCTGGAATGCAACTTCGGCGCCAGCTCCACCGCTCTGAAGGGGATCTG
HL.FBE49R   ACCACACCAAGGGGCTGGAATGCAACTTCGGCGCCAGCTCCACCGCTCTGAAGGGGATCTG
HL.FBEXXR2A   ACCACACCAAGGGGCTGGAATGCAACTTCGGCGCCAGCTCCACCGCTCTGAAGGGGATCTG
HL.FBEXXR2   GCCAGCTCCACCGCTCTGAAGGGGATCTG
#367
              _____

              ACCACACCAAGGGGCTGGAATGCAACTTCGGCGCCAGCTCCACCGCTCTGAAGGGGATCTG

HL.FBEXXRA   CAGAGCTCAGTCAGAGGGCAGACCCTGTGAATATAACTCCAGAATCTACCAAAACGGGGAA
HL.FBEXXR   CAGAGCTCAGTCAGAGGGCAGACCCTGTGAATATAACTCCAGAATCTACCAAAACGGGGAA
HL.FBE49XX   CAGAGCTCAGTCAGAGGGCAGACCCTGTGAATATAACTCCAGAATCTACCAAAACGGGGAA
HL.FBE49R   CAGAGCTCAGTCAGAGGGCAGACCCTGTGAATATAACTCCAGAATCTACCAAAACGGGGAA
HL.FBEXXR2A   CAGAGCTCAGTCAGAGGGCAGACCCTGTGAATATAACTCCAGAATCTACCAAAACGGGGAA
HL.FBEXXR2   CAGAGCTCAGTCAGAGGGCAGACCCTGTGAATATAACTCCAGAATCTACCAAAACGGGGAA
#428
              _____

              CAGAGCTCAGTCAGAGGGCAGACCCTGTGAATATAACTCCAGAATCTACCAAAACGGGGAA

HL.FBEXXRA   AG
HL.FBEXXR   AGTTTCCAGCCCAACTGT
HL.FBE49XX   AGTTTCCAGCCCAACTGTAAACATCAGTGCACATGTATTGGATGGCGCCGGGGGGCTTGCA
HL.FBE49R   AGTTTCCAGCCCAACTGTAAACATCAGTGCACATGTATTG:ATGGCGCCGTGGG:CT:GCA
HL.FBEXXR2A   AGTTTCCAGCCCAACTGTAAACATCAGTGCACATGTATTG:ATGGCGCCGTGGG:CT:GCA
HL.FBEXXR2   AGTTTCCAGCCCAACTGTAAACATCAGTGCACATGTATTG:ATGGCGCCGTGGG:CT:GCA
HL.FBEXXR2BA   CATCAGTGCACATGTATTG:ATGGCGCCGTGGG:CT:GCA
HL.FBEXXR2B   TCAGTGCACATGTATTG:ATGGCGCCGTGGG:CT:GCA
#489
              _____

              AGTTTCCAGCCCAACTGTAAACATCAGTGCACATGTATTG:ATGGCGCCGTGGG:CT:GCA

HL.FBE49XX   TTCCTCTGTGTCCCCAAGAACTATCTCTCCCCAACTTGGGCTGTCCCAACCCTCGGCTGGT
HL.FBE49R   TTCCTCTGTGTCCCCAAGAACTATCTCTCCCCAACTTGGGCTGTCCCAACCCTCGGCTGGT
HL.FBEXXR2A   TTCCTCTGTGTCCCCAAGAACTATCTCTCCCCAACTTGGGCTGTCCCAACCCTCGGCTGGT
HL.FBEXXR2   TTCCTCTGTGTCCCCAAGAACTATCTCTCCCCAACTTGGGCTGTCCCAACCCTCGGCTGGT
HL.FBEXXR2BA TTCCTCTGTGTCCCCAAGAACTATCTCTCCCCAACTTGGGCTGTCCCAACCCTCGGCTGGT
HL.FBEXXR2B   TTCCTCTGTGTCCCCAAGAACTATCTCTCCCCAACTTGGGCTGTCCCAACCCTCGGCTGGT
#550
              _____

              TTCCTCTGTGTCCCCAAGAACTATCTCTCCCCAACTTGGGCTGTCCCAACCCTCGGCTGGT

HL.FBE49XX   CAAAGTTACCGGGCAGTGCTGCGAGGAGTGGGTCTGTGACGAGGATAGTATCAAGGACCCC
HL.FBE49R   CAAAG
HL.FBEXXR2A   CAAAGTTACCGGGCAGTGCTGCGAGGAGTGGGTCTGTGACGAGGATAGTATCAAGGACCCC
HL.FBEXXR2   CAAAGTTACCGGGCAGTGCTGCGAGGAGTGGGTCTGTGACGAGGATAGTATCAAGGACCCC
HL.FBEXXR2BA CAAAGTTACCGGGCAGTGCTGCGAGGAGTGGGTCTGTGACGAGGATAGTATCAAGGACCCC
HL.FBEXXR2B   CAAAGTTACCGGGCAGTGCTGCGAGGAGTGGGTCTGTGACGAGGATAGTATCAAGGACCCC
HL.FBEXXR3   GAGGATAGTATCAAGGACCCC
#611
              _____

              CAAAGTTACCGGGCAGTGCTGCGAGGAGTGGGTCTGTGACGAGGATAGTATCAAGGACCCC

HLFBE49XX	ATGGAGGACCAGGACGGCCTCCTTGGCAAGGGGCTGGGGATTCGATGCCTCCGAGGTGGAGT
HLFBEXXR2A	ATGGAGGACCAGGACGGCCTCCTTGGCAAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGT
HLFBEXXR2	ATGGAGGACCAGGACGGCCTCCTTGGCAAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGT
HLFBEXXR2BA	ATGGAGGACCAGGACGGCCTCCTTG
HLFBEXXR2B	ATGGAGGACCAGGACGGCCTCCTTGGCAAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGT
HLFBEXXR3	ATGGAGGACCAGGACGGCCTCCTTGGCAAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGT
HLFBEXXR3BA	GATGCC TCCGAGGTGGAGT
HLFBEXXR3B	TGCC TCCGAGGTGGAGT

#672

ATGGAGGACCAGGACGGCCTCCTTGGCAAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGT

HLFBE49XX	TGACGAGAAACAATGAATTGATTGCAGTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGT
HLFBEXXR2A	TGACGAGAAACAATGAATTGATTGCAGTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGT
HLFBEXXR2	TGACGAGAAACAATGAATTGATTGCAGTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGT
HLFBEXXR2B	TGACGAGAAACAATGAATTGATTGCAGTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGT
HLFBEXXR3	TGACGAGAAACAATGAATTGATTGCAGTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGT
HLFBEXXR3BA	TGACGAGAAACAATGAATTGATTGCAGTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGT
HLFBEXXR3B	TGACGAGAAACAATGAATTGATTGCAGTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGT

#733

TGACGAGAAACAATGAATTGATTGCAGTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGT

HLFBE49XX	TTTTGGAATGGAGCCTCGCATCCTATACAACCCTTTACAAGGCCAGAAATGTATTGTTCAA
HLFBEXXR2A	TTTTGGAATGGAGCCTCGCATCCTATACAACCCTTTACAAGGCCAGAAATGTATTGTTCAA
HLFBEXXR2	TTTTGGAATGGAGCCTCGCATCCTATACAACCCTTTACAAGGCCAGAAATGTATTGTTCAA
HLFBEXXR2B	TTTTGGAATGGAGCCTCGCATCCTATACAACCCTTTACAAGGCCAGAAATGTATTGTTCAA
HLFBEXXR3	TTTTGGAATGGAGCCTCGCATCCTATACAACCCTTTACAAGGCCAGAAATGTATTGTTCAA
HLFBEXXR3BA	TTTTGGAATGGAGCCTCGCATCCTATACAACCCTTTACAAGGCCAGAAATGTATTGTTCAA
HLFBEXXR3B	TTTTGGAATGGAGCCTCGCATCCTATACAACCCTTTACAAGGCCAGAAATGTATTGTTCAA

#794

TTTTGGAATGGAGCCTCGCATCCTATACAACCCTTTACAAGGCCAGAAATGTATTGTTCAA

HLFBE49XX	ACAACTTCATGGTCCCAGTGCTCAAAGACCTGTGGAACTGGTATCTCCACACGAGTTACCA
HLFBEXXR2A	ACAACTTCATGGTCCCAGTGCTCAAAGACCTGTGGAACTGGTATCTCCACACGAGTTACCA
HLFBEXXR2	ACAACTTCATGGTCCCAGTGCTCAAAGACCTGTGGAACTGGTATCTCCACACGAGTTACCA
HLFBEXXR2B	ACAACTTCATGGTCCCAGTGCTCAAAGACCTGTGGAACTGGTATCTCCACACGAGTTACCA
HLFBEXXR3	ACAACTTCATGGTCCCAGTGCTCAAAGACCTGTGGAACTGGTATCTCCACACGAGTTACCA
HLFBEXXR3BA	ACAACTTCATGGTCCCAGTGCTCAAAGACCTGTGGAACTGGTATCTCCACACGAGTTACCA
HLFBEXXR3B	ACAACTTCATGGTCCCAGTGCTCAAAGACCTGTGGAACTGGTATCTCCACACGAGTTACCA
HLFBEXXR4A	GTATCTCC ACACGAGTTACCA
HLFBEXXR4	AT CTCCAC ACGAGTTACCA

#855

ACAACTTCATGGTCCCAGTGCTCAAAGACCTGTGGAACTGGTATCTCCACACGAGTTACCA

HLFBE49XX   ATGACAACCCTGAGTGCCGCCTTGTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGG
HLFBEXXR2A   ATGACAACCCTGAGTGCCGCCTTGTGAAAGAAACCC
HLFBEXXR2   ATGACAACCCTGAGTGCCGCC TTGTGAAAGAAAC CCGG ATTTGTGAGGTG CGGC CTTGTGG
HLFBEXXR2B   ATGACAACCCTGAGTGCCGCCTTGTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGG
HLFBEXXR3   ATGACAACCCTGAGTGCCGCCTTGTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGG
HLFBEXXR3BA   ATGACAACCCTGAGTGCCGCCTTGTGAAAGAAACCCGGATTTGTG AGGTGC GGCCTTGTGG
HLFBEXXR3B   AT
HLFBEXXR4A   ATGACAACCCTGAGTGCCGCCTTGTGAAAGAAACCCGGATTTGTG AGGTGCGGCC TTGTGG
HLFBEXXR4   ATGACAACCCTGAGTGCCGCCTTGTGAAAGAAACCCGGATTTGTGAGGTGCGGCC TTGTGG
HLFBEXXR4B   GCC TTGTG AAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGG
              _____
#916
              ATGACAACCCTGAGTGCCGCCTTGTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGG

HLFBE49XX   ACAGCCAGTGTACAGCAGCCTGAAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCC
HLFBEXXR2   ACAGCCAGTGTACAGCAGCCTGAAAAAGGGCAAG AAATGCAGCAAGACCAAGAAATCCCC C
HLFBEXXR2B   ACAGCCAGTGTACAGCAGCCTGAAAAAG GGCAAGAAATGCAGCAAGACCAAGAAATCCCCC
HLFBEXXR3   ACAGCCAGTGTACAGCAGCCTGAAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCC
HLFBEXXR3BA   ACAGCCAGTGTACAGCAGCCTGAAAAAGGGCAAG AAATGCAGC AAG ACCAAGAAATCCCCC
HLFBEXXR4A   ACAGCC AGTG TACAGCAGCCTGAAAAA GG GCAAG AAATGCAGC AAGACCAAGAAATCCCCC
HLFBEXXR4   ACAGCC AGTGTACAGCAGCCTGAAAAA GGGCAAG AAATGCAGC AAGACCAAGAAATCCCCC
HLFBEXXR4B   ACAGCCAGTGTACAGCAGCCTGAAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCC
              _____
#977
              ACAGCCAGTGTACAGCAGCCTGAAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCC

HLFBE49XX   GAACCAGTCAGGTTTACTTACGCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACT
HLFBEXXR2   GAA CCAGTCAGGTTTACTTACGCTGGATGTT TGAGTGTGAAGAAATACCGGCC CAAGTAC T
HLFBEXXR2B   GAACCAGTCAGGTTTACTTACGCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACT
HLFBEXXR3   GAACCAGTCAGGTTTACTTACGCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACT
HLFBEXXR3BA   GAACCAGTCAGGTTTACTTACGCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACT
HLFBEXXR4A   GAA CCAGTC AGG TTTAC TTACGCTGGA TGTTTGAGTGTGA AGAAATACCGGCC CAAG TACT
HLFBEXXR4   GA ACCAGTCAGG TTTACTTACGCTGGA TGTTTGAGTGTGA AGAAATACCGGCC CAAGTACT
HLFBEXXR4B   GAACCAGTCAGGTTTACTTACGCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACT
              _____
#1038
              GAACCAGTCAGGTTTACTTACGCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACT

HLFBE49XX   GCGGTTCCTGCGTGGACGGCCGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCG
HLFBEXXR2   GCG GTTC CTGCGTGGACGGCCGATGCTGCACGCCCCAGC TGACCAGGACTGTGAAGATGCG
HLFBEXXR2B   GCGGTTCCTGCGTGGACGGCCGATGCTGCACGCCCC
HLFBEXXR3   GCGGTTC CTGCGTGGACGGCCGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCG
HLFBEXXR3BA   GCG GTTCCTGCGTGGACGGCCGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCG
HLFBEXXR4A   GCGGTTC CTGC GTG GACGG CC GATGC TGC ACGCCCAGC TGACCAGGA CTGTG AAGA TGCG
HLFBEXXR4   GCGGTTC CTGCGTG GACGG CCGATGC TGC ACGCCCCAGC TGACCAGGA CTGTG AAGA TGCG
HLFBEXXR4B   GCGGTTCCTGCGTGGACGGCCGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCG
HLFBEXXR5   CC GATGCTGCAC GC CCCAGCT GACCAG GACTGTGAAGATGCG
HLFBEXXR5A   TGC TG CACGC CCCAG CTGACCAG GACTGTGAAGATGCG
              _____
#1099
              GCGGTTCCTGCGTGGACGGCCGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCG

HL.FBE49XX   GTTCCCCTGCGAAGATGGGGAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTCCAAA
HL.FBEXXR2   GTTCCGCT GCGAAGAT GGGGAG ACAT TTTCCAAGA ACGTC ATGATGA TCCAGTCCT
HL.FBEXXR3   GTTCCGCTGCGAAGATGGGGAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAA
HL.FBEXXR3BA   GTTCCGCTGCGAAGA TGGGGAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAA
HL.FBEXXR4A   GTTCCGCTGCGAAGA
HL.FBEXXR4   GTTCCGCTGCGAAGA
HL.FBEXXR4B   GTTCCGCTGCGAAGATGG
HL.FBEXXR5   GTTCCGCTGCGAAGATGGGGAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAA
HL.FBEXXR5A   GTTCCGCTGCGAAGATGGGGAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAA
    #1160   _____

                GTTCCGCTGCGAAGATGGGGAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAA

HL.FBE49XX   TGCAACTACAACTGCCCGCATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCCAAT
HL.FBEXXR3   TGCAACTACAACTGCCCGCATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTC:AAT
HL.FBEXXR3BA   TGCAACTACAACTGCCCGCATGCCAATGAAGCAGC GTTTCCCTTCTACAGGCTGTTC:AAT
HL.FBEXXR5   TGCAACTACAACTGCCCGCATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTC:AAT
HL.FBEXXR5A   TGCAACTACAACTGCCCGCATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTC:AAT
HL.FBEXXF   TCCCTTCTACAGGCTGTTC:AAT
    #1221   _____

                TGCAACTACAACTGCCCGCATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTC:AAT

HLFBE49XX   GACATTCACAAATTTAGGGACTAAATGCTACCTGGGTTTCCAGGGCACACCTAGACCAAAC
HLFBEXXR3   GACATTCACAAATTTAGGGACTAAATGCTACCTGGGTTTCCAGGGCACACCTAGAC:AAAC
HLFBEXXR3BA   GACATTCACAAATTTAGGGACTAAATGCTACCTGGGTTTCCAGGGCACACCTAGAC:AAAC
HLFBEXXR5   GACATTCACAAATTTAGGGACTAAATGCTACCTGGGTTTCCAGGGCACACCTAGAC:AAAC
HLFBEXXR5A   GACATTCACAAATTTAGGGACTAAATGCTACCTGGGTTTCCAGGGCACACCTAGAC:AAAC
HLFBEXXF   GAC ATTC AC AAATTTAGG GGACTAAATGCTACCTGGGTTTCCAGGGCACACCTAGAC:AAAC
    #1282   _____

                GACATTCACAAATTTAGGGACTAAATGCTACCTGGGTTTCCAGGGCACACCTAGAC:AAAC

HLFBE49XX   AAGGGAGAAGAGTGTCAGAATCAGAATCATGGAGAAAATGGGCGGGGGTGGTGTGGGTGAT
HLFBEXXR3   AAGGGAGAAGAGTGTCAGAATCAGAATCATGGAGAAAATGG
HLFBEXXR3BA   AAGGGAGAAGAG
HLFBEXXR5   AAGGGAGAAGAGTGTCAGAATCAGAATCATGGAGAAAATGGGCGGNGGTGGTGTGGGTGAT
HLFBEXXR5A   AAGGGAGAAGAGTGTCAGAATCAGAATCATGGAGAAAATGGGCGGNGGTGGTGTGGGTGAT
HLFBEXXF   AAGGGAGAAGAGTGTCAGAATCAGAATCATGGAGAAAATGGGCGGGGGTGGTGTGGGTGAT
HLFBEXXR6BA   GGGAN NAGAGT GTCAGAATCAGAATCN TGGAGAAAATGGGCGGGGGTGGTGTGGGTGAT
HLFBEXXR6B   GTCAG AATNAGA ATCA TGGANAAAATGGGCGGNGGTGGTGTGGGTGAT
HLFBEXXR6   AAAATGGNCGGNGGTGGTGTGGGTGAT
    #1343   _____

                AAGGGAGAAGAGTGTCAGAATCAGAATCATGGAGAAAATGGGCGGGGGTGGTGTGGGTGAT
                ++   +   +   +   +   +

HLFBE49XX   GGGACTCATTGTAGAAAGGAAGCCTTGCTCATTCTTGAGGAGCATTAAGGTATTTCGAAAC
HLFBEXXR5   GGGACTCATTGTAGAAAGGAAGCCTTGCTCATTCTTGAGGAGCATTAAGGTATTTCGAAAC
HLFBEXXR5A   GGGACTCATTGTAGAAAGGAAGCCTTGCTCATTCTTGAGGAGCATTAAGG TATTTCGAAAC
HLFBEXXF   GGGACTCATTGTAGAAAGGAAGCCTTGCTCATTCTTGAGGAGCATTAAGGTATTTCGAAAC
HLFBEXXR6BA GGGACTCATTGTAGAAAGGAAGCCTTGCTCATTCTTGAGGAGCATTAAGGTATTTCGAAAC
HLFBEXXR6B   GGGACTCATTGNAGAAAGGAAGCCTTGCTCATTCTTGAGGAGCATTAANGTATTTCNAAAC
HLFBEXXR6   GGGACTCATTGTAGAAAGGAAGCCTTGCTCATTCTTGAGGAGCATTAAGG TATTTCGAAAC
HLFBEXXR6A   ACTCANTGTAGAAAGGAAGCCTTGCTNATTNTTGAGGAGCATTANGG TAT TTNGAAAC
HLFBEXXFA   AGGTATTTCGAAAC

#1404

             GGGACTCATTGTAGAAAGGAAGCCTTGCTCATTCTTGAGGAGCATTAAGGTATTTCGAAAC
                       +   +   +   +   ++   ++

HLFBE49XX   TCCCAAGGGTGCTGGTGCGGATGGACACTAATGCAGCCACGATTGGAGAATACTTTGCTTC
HLFBEXXR5   TGCCAAGGGTGCTGGTGCGGATGGACACTAATGCAGCCACGATTGGAGAATACTTTGCTTC
HLFBEXXR5A   TGCCAAGGGTGCTGGTGCGGATGGACACTAATGCAGCCACGATTGGAGAATACTTTGCTTC
HLFBEXXF   TGCCAAGGGTGCTGGTGCGGATGGACACTAATGCAGCCACGATTGGAGAATACTTTGCTTC
HLFBEXXR6BA TGCCAAGGGTGCTGGTGCGGATGGACACTAATGCAGCCACGATTGGAGAATACTTTGCTTC
HLFBEXXR6B   TGCCAAGGGTGCTGGTGCGGATGGACACTAATGCAGCCACGATTGGAGAATACTTTGCTTC
HLFBEXXR6   TGCCAAGGGTGCTGGT GCGGATGGACACTAATGCAGCCACGATTGGAGAATACTTTGCTTC
HLFBEXXR6A   TGCCAAGGGTGCTGGTGNGGATGGACACTA
HLFBEXXFA   TGCCAAGGGTGCTGGTGCGGATGGACACTAATGCAGCCACGATTGGAGAATACTTTGCTTC

#1465

             TGCCAAGGGTGCTGGTGCGGATGGACACTAATGCAGCCACGATTGGAGAATACTTTGCTTC
                     .   +

HLFBE49XX   ATAGTATTGGAGCACATGTTACTGCTTCATTTTGGAGCTTGTGGAGTTGATGACTTTCTGT
HLFBEXXR5   ATAGTATTGGAGCACATGTTACTGCTTCATTTTGGAGCTTGTGGAGTTGATGACTTTCTGT
HLFBEXXR5A   ATAGTATTGGAGCACATGTTACTGCTTCATTTTGGAGCTTGTGGAGTTGATGACTTTCTGT
HLFBEXXF   ATAGTATTGGAGCACATGTTACTGCTTCATTTTGGAGCTTGTGGAGTTGATGACTTTCTGT
HLFBEXXR6BA ATAGTATTGGAGCACATGTTACTGCTTCATTTTGGAGCTTGTGGAGTTGATGACTNTCTGT
HLFBEXXR6B   ATAGTATTGGAGCACATGTTACTGCTTCATTTTGGAGCTTGTGGAGTTGATGACTTTCTGT
HLFBEXXR6   ATAGTATTGGAGCACATGTTACTGCTTCATTTTGGAGCTTGTGGAGNTGATGACTNTCTGT
HLFBEXXFA   ATAGTATTGGAGCACATGTTACTGCTTCATTTTGGAGCTTGTGGAGTTGATGACTTTCTGT
HLFBEXXR7A   TGT

#1526

             ATAGTATTGGAGCACATGTTACTGCTTCATTTTGGAGCTTGTGGAGTTGATGACTTTCTGT
                                                            +   +

HLFBE49XX   TTTCTGTTTGTAAATTATTTGCTAAGCATATTTTCTCTAGGCTTTTTTCCTTTTGGGGTTC
HLFBEXXR5   TTTCTGTTTGTAAATTATTTGCTAAGCATATTTTCTCTAGGCTTTTTTCCTTTTGGGGTTC
HLFBEXXR5A   TTTCTGNTTGTAAATTATTTGCTAAGCATATTTTCTCTAGGCTTTTTTCCTTTTGGGGTTC
HLFBEXXF   TTTCTGTTTGTAAATTATTTGCTAAGCATATTTTCTCTAGGCTTTTTTCCTTTTGGGGTTC
HLFBEXXR6BA TNTCTGTTTGTAAATTATTTGCTAAGCATATTTTCTCTAGGCTTTTTTCCTTTTGGGGTTC
HLFBEXXR6B   TTTCTGTTTGTAAATTATTTGNTAANCATATTTNCTCTAGGCTTTTTTCCTTTTGGGGTTC
HLFBEXXR6   TTTCTGNTNGT
HLFBEXXFA   TTTCTGTTTGTAAATTATTTGCTAAGCATATTTTCTCTAGGCTTTTTTCCTTTTGGGGTTC
HLFBEXXR7A   TNTCTGTTTGTAAATTATTNGCTAAGCATATTTTCTCTAGGCTNTTTTCCTTTTGGGGTTC

#1587

             TTTCTGTTTGTAAATTATTTGCTAAGCATATTTTCTCTAGGCTTTTTTCCTTTTGGGGTTC
               +   + +   + +   +   +   +

HL.FBE49XX   TACAGTCGTAAAAGAGATAATAAGATTAGTTGGACAGTTTAAAGCTTTTATTCGTCCTTTG
HL.FBEXXR5   TACAGTCGTAAAAGAGATAATAAGATTAGTTGGACAGTTTAAAGCTTTTATTCGTCCTTTG
HL.FBEXXR5A   TACAGTCGTAAAAGAGATAATAAGATTAGTTGGACAGTTTAAAGCTTTTATTCGTNCTTTG
HL.FBEXXF   TACAGTCGTAAAAGAGATAATAAGATTAGTTGGACAGTTTAAAGCTTTTATTCGTCCTTTG
HL.FBEXXR6BA   TACAGTCGTAAAAGAGATAATAAGATTAGTTGGACAGNTTAAAGCTTTTATTCGTCCTTTG
HL.FBEXXR6B   TACAGTNGTAAAAGAGATAATAAGATTAGTTGNACAGTTNAAAGCTTTTATTCGTCCTTTG
HL.FBEXXFA   TACAGTCGTAAAAGAGATAATAAGATTAGTTGGACAGTTTAAAGCTTTTATTCGTCCTTTG
HL.FBEXXR7A   TACAGTCGTAAAAGAGATAATAAGATTAGTTGGACAGTTTAAAGCTTTTATTCGTCCTTTG
#1648   --

                TACAGTCGTAAAAGAGATAATAAGATTAGTTGGACAGTTTAAAGCTTTTATTCGTCCTTTG
                   +   +   + +   +

HL.FBE49XX   ACAAAAGTAAATGGGAGGGCATTCCATCCCTTCCTGGAGGGGGACACTCCATGAGTGTCTG
HL.FBEXXR5   ACAAAAGTAAATGGGAGGGCATTCCATCCCTTCCTGAAGGGGGACACTCCATGAGTGTCTG
HL.FBEXXR5A   ACAAAAGTAAATGGGAGGGCATTCCATCCCTTCCTGAAGGGGGACACTCCATGAGTGTCTG
HLFBEXXF   ACAAAAGTAAATGGGAGGGCATTCCATCCCTTCCTGAAGGGGGACACTCCATGAGTGTCTG
HLFBEXXR6BA   ACAAAAGTAAATGGGAGGGCATTCCATCCCTTCCTGAAGGGGGACACTCCATGAGTGTCTG
HLFBEXXR6B   ACANAAGTNAATGGGAGGGCATTCCATCCCTTCCTGAAGGGGGACACTCCATGAGTGTCTG
HLFBEXXFA   ACAAAAGTAAATGGGAGGGCATTCCATCCCTTCCTGAAGGGGGACACTCCATGAGTGTCTG
HLFBEXXR7A   ACAAAAGTAAATGGGAGGGCATTCCATCCCTTCCTGAAGGGGGACACTCCATGAGTGTCTG
#1709   --

                ACAAAAGTAAATGGGAGGGCATTCCATCCCTTCCTGAAGGGGGACACTCCATGAGTGTCTG
                   +   +   .

HLFBE49XX   TGAGAGGCAGCTATCTGCACTCTAAACTGCAAACAGAAATCAGGTGTTTTAAGACTGAATG
HLFBEXXR5   TGAGAGGCAGCTATCTGCACTCTAAACTGCAAACAGAAATCAGGTGTT TTAAGACTGAATG
HLFBEXXR5A   TGAGAGGCAGCTATCTGCACTCTAAACTGCAAACAGAAATCANGTGTT TTAAGACTGAATG
HLFBEXXF   TGAGAGGCAGCTATCTGCACTCTAAACTGCAAACAGAAATCAGGTGTTTTAAGACTGAATG
HLFBEXXR6BA   TGAGAGGCAGCTATCTGCACTCTAAACTGCAAACAGAAATCAGGTGTTTTAAGACTGAATG
HLFBEXXR6B   TGAGAGGCAGCTATCTGCACTCTAAACTGCANNCAGAAATCAGGTG TTTTAAGACTGAANG
HLFBEXXFA   TGAGAGGCAGCTATCTGCACTCTAAACTGCAAACAGAAATCAGGTGTTTTAAGACTGAATG
HLFBEXXR7A   TGAGAGGCAGCTATCTGCACTCTAAACTGCAAACAGAAATCAGGTGTTTTAAGACTGAATG
HLFBEXXR8   CTGNAAACAGANATCAGGTGTTTTAAGACTGAATG
HLFBEXXR8A   AAACAGAAATCAGGTGTTTTAAGACTGAATG
#1770   --

                TGAGAGGCAGCTATCTGCACTCTAAACTGCAAACAGAAATCAGGTGTTTTAAGACTGAATG
                                        + ++   +   +   +

HLFBE49XX   TTTTATTTATCAAAATGTAGCTTTTGGGGAGGGAGGGGAAATGTAATACTGGAATAATTTG
HLFBEXXR5   TTTTATTTATCAAAATGTAGC TTTTGGGGAGGNAGGGGAAATGNAATACTGGAATAATTTG
HLFBEXXR5A   TTTTATTTATCAAAATGTAGC TTTTGGGGAGGGAGGGGAAATGTAATACTGGAATAATTTG
HLFBEXXF   TTTTATTTATCAAAATGTAGCTTTTGGGGAGGGAGGGGAAATGTAATACTGGAATAATTTG
HLFBEXXR6BA   TTTTATTTATCAAAATGTAGCTTTTGGGGAGGGAGGGGAAATGTAATACTGGAATAATTTG
HLFBEXXR6B   TTTTATTTATC
HLFBEXXFA   TTTTATTTATCAAAATGTAGCTTTTGGGGAGGGAGGGGAAATGTAATACTGGAATAATTTG
HLFBEXXR7A   TTTTATTTATCAAAATGTAGCTTTTGGGGAGGGAGGNGAAATGTAATACTGGNATAATTTG
HLFBEXXR8   TTTTATTTATCAAAATGTAGCTTTTGGGGAGGGAGGGGAAATGTAATACTGGAATAATTTG
HLFBEXXR8A   TTTTATTTATCAAAATGTAGCTTTTGGGGAGGGAGGGGAAATGTAATACTGGAATAATTTG
#1831   --

                TTTTATTTATCAAAATGTAGCTTTTGGGGAGGGAGGGGAAATGTAATACTGGAATAATTTG
                                   +   +   +   +

HL.FBE49XX   TAAATGATTTTAATTTTATATTCAGTGAAAAGATTTTATTTATGGAATTAACCATTTAATA

HL.FBEXXR5   TAAATGATTTTAATTTTATATTCAGTGAAAAGATTTTATTTATGGAATTAACCATTTAATA

HL.FBEXXR5A   TAAANGATTTTAATTTT

HL.FBEXXF   TAAATGATTTTAATTTTATATTCAGTGAAAAGATTTTATTTATGGAATTAACCATTTAATA

HL.FBEXXR6BA   TAAATGATTTTAATTTTATATTCAGTGAAAAGATTTTATTTATGGAATTAACCATTTAATA

HL.FBEXXFA   TAAATGATTTTAATTTTATATTCAGTGAAAAGATTTTATTTATGGAATTAACCATTTAATA

HL.FBEXXR7A   TAAATGATTTTAATTTTATATTCAGNGAAAAGATTTTA

HL.FBEXXR8   TAAATGATTTTAATTTTATATTCAGTGAAAAGATTTTATTTATGGAATTAACCATTTAATA

HL.FBEXXR8A   TAAATGATTTTAATTTTATATTCAGTGAAAAGATTTTATTTATGGAATTAACCATTTAATA

        #1892   _____

                   TAAATGATTTTAATTTTATATTCAGTGAAAAGATTTTATTTATGGAATTAACCATTTAATA
                      +   +

HL.FBE49XX   AAGAAATATTTACCTAAAAAAAAAAAAAAAAAAAAAA

HL.FBEXXF   AAGAAATATTTACCTAAAAAAAAAAAAAAAAAAAAAAAAA

HL.FBEXXR6BA   AAGAAATATTTACCTAA

HL.FBEXXFA   AAGAAATATTTACCTAAAAAAAAAAAAAAAAAAAAAAAA

HL.FBEXXR8   AAGAAATATTTACCTAAAAAAAAAAAAAAAAAAAAAAAA

HL.FBEXXR8A   AAGAAATATTTACCTAAAAAAAAAAAAAAAAAAAAAAAA

        #1953   _____

                   AAGAAATATTTACCTAAAAAAAAAAAAAAAAAAAAAAAA

```
  1  ATGAGCTCCCGCATCGCCAGGGCGCTCGCCCTTAGTCGTCACCCTTCTCCACTTGACCAGG   60
  1   M  S  S  R  I  A  R  A  L  A  L  V  V  T  L  L  H  L  T  R    20


 61  CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG   120
 21   L  A  L  S  T  C  P  A  A  C  H  C  P  L  E  A  P  K  C  A    40


121  CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC   180
 41   P  G  V  G  L  V  R  D  G  C  G  C  C  K  V  C  A  K  Q  L    60


181  AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC   240
 61   N  E  D  C  S  K  T  Q  P  C  D  H  T  K  G  L  E  C  N  F    80


241  GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT   300
 81   G  A  S  S  T  A  L  K  G  I  C  R  A  Q  S  E  G  R  P  C   100


301  GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG   360
101   E  Y  N  S  R  I  Y  Q  N  G  E  S  F  Q  P  N  C  K  H  Q   120


361  TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC   420
121   C  T  C  I  D  G  A  V  G  C  I  P  L  C  P  Q  E  L  S  L   140


421  CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG   480
141   P  N  L  G  C  P  N  P  R  L  V  K  V  T  G  Q  C  C  E  E   160
```

FIG. 1A

481 TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC 540
161 W   V   C   D   E   D   S   I   K   D   P   M   E   D   Q   D   G   L   L   G 180

541 AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA 600
181 K   E   L   G   F   D   A   S   E   V   E   L   T   R   N   N   E   L   I   A 200

601 GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA 660
201 V   G   K   G   S   S   L   K   R   L   P   V   F   G   M   E   P   R   I   L 220

661 TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA 720
221 Y   N   P   L   Q   G   Q   K   C   I   V   Q   T   T   S   W   S   Q   C   S 240

721 AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT 780
241 K   T   C   G   T   G   I   S   T   R   V   T   N   D   N   P   E   C   R   L 260

781 GTGAAAGAAACCCGGATTTGTGAGGTGCCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG 840
261 V   K   E   T   R   I   C   E   V   R   P   C   G   Q   P   V   Y   S   S   L 280

841 AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC 900
281 K   K   G   K   K   C   S   K   T   K   K   S   P   E   P   V   R   F   T   Y 300

901 GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC 960
301 A   G   C   L   S   V   K   K   Y   R   P   K   Y   C   G   S   C   V   D   G 320

FIG. 1B

```
 961  CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG  1020
 321  R   C   C   T   P   Q   L   T   R   T   V   K   M   R   F   R   C   E   D   G   340
```

```
1021  GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG  1080
 341  E   T   F   S   K   N   V   M   M   I   Q   S   C   K   C   N   Y   N   C   P   360
```

```
1081  CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG  1140
 361  H   A   N   E   A   A   F   P   F   Y   R   L   F   N   D   I   H   K   F   R   380
```

```
1141  GACTAA  1146
 381  D   *   382
```

FIG. 1C

FIG. IA

```
ATGAGCTCCGCATCGGCAGGAAGCTCGGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG
 M  S  S  R  I  A  R  K  L  A  L  V  V  T  L  L  H  L  T  R

CTGGCGGCTCTCCACCTGCCCGCTCCTGCCCCCTGGAGGGCGCCAAGTGCGCG
 L  A  L  S  T  C  P  A        C  H  C  P  L  E  A  P  K  C  A

CCGGGGAGTCGGGTCCGGGTCCGGGTTGGCGGCTGTGTTGTTGCCCAAGCAGCTC
 P  G  V  G  L  V  R  D  G  G  C  C  K  V  C  A  K  Q  L

AACGAGGACTGCAAGAAAAACGCAGCCCTGCCGACCACCACCAAGGGGGGCTGGAATGCAACTTC
 N  E  D  C  K  T  Q  P  C  D  H  T  K  G  L  E  C  N  F

GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGGCGAGACCCTGT
 G  A  S  T  A  L  K  G  I  C  R  A  Q  S  E  G  R  P  C

GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCAAACTGTAAACATCAG
 E  Y  N  S  R  I  Y  Q  N  G  E  S  F  Q  P  N  C  K  H  Q

TGCACATGTATTGGAATGGCGCGCGGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCT
 C  T  I        C  I  P  L  C  P  Q  E  L  S

CTCCCCAACTTGGGGTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAG
 L  P  N  L  G  C  P  N  P  R  L  V  K  V  T  G  Q  C  C  E
```

MATCH WITH FIG. 1B

FIG. IB

```
          .                   .                   .                   .
GAGTGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGGCCTCCTT
 E  W  V  C  D  E  D  S  I  K  D  P  M  E  D  Q  D  G  L  L

          .                   .                   .                   .
GGCAAGGCGGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATT
 G  K     G  L  G  F  D  A  S  E  V  E  L  T  R  N  E  L  I
    E

          .                   .                   .                   .
GCAGTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCCTGTTTTTTGGAATGGAGCCTCGCATC
 A  V  G  K  G  S  S  L  K  R  L  P  V  F  G  M  E  P  R  I

          .                   .                   .                   .
CTATACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGC
 L  Y  N  P  L  Q  G  Q  K  C  I  V  Q  T  S  V  S  Q  C

          .                   .                   .                   .
TCAAAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGC
 S  K  T  G  I  S  T  R  V  T  N  D  N  P  E  C  R

          .                   .                   .                   .
CTTGTGAAAGAAACCCGGATTTGTGAGGTGCGGGCCTTGTGGACAGCCAGTGTACAGCAGC
 L  V  K  E  T  R  I  C  E  V  R  P  C  G  Q  P  V  Y  S  S

          .                   .                   .                   .
CTGAAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCGAACCAGTCAGGTTTTACT
 L  K  K  G  K  K  C  S  K  T  K  K  S  P  E  P  V  R  F  T
```

FIG. 1C

```
TACGCTGGATGTTTGAGTGTGAAGAATACCGGCCCAAGTACTGCGGGTTCCTGCGTGGAC
Y  A  G  C  L  S  V  K  K  Y  R  P  K  Y  C  G  S  C  V  D

GGCCGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCCTGCGAAGAT
G  R  C  C  T  P  Q  L  T  R  T  V  K  M  R  F  C  E  D

GGGGAGACATTTTCCAAGAAGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGC
G  E  T  F  S  K  N  V  M  M  I  Q  S  C  K  C  N  Y  N  C

CCGCATGCCAATGAAGCAGCGTTTCCTTACAGGCTGTTTCAATGACATTCACAAA
P  H  A  N  E  A  A  F  F  Y  R  L  F  ...

TTTAGGGACTAA
F  R  D  *
```

FIG. 2A

```
  1 MSSRIVRELALVVTLLHLTRVGLSTCPADCHCPLEAPKCAPGVGLVRDGC  50
    |||...|..||:..||::||||||||||||||||||||||||||||
  1 MSSSTFRTLAVAVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGC  50

 51 GCCKVCAKQLNEDCRKTQPCDHPKGLECNFGASSTALKGICRAQSEGRPC 100
    |||||||||||||||  |||  ||||||||||||||||||||||
 51 GCCKVCAKQLNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPC 100

101 EYNSRIYQNGESFQPNCKHQCTCIGWRRGACIPLCPQELSLPNLGCPNPR 150
```

MATCH WITH FIG. 2B

MATCH WITH FIG. 2A

FIG. 2B

```
101 EYNSRIYQNGESFQPNCKHQCTCID.GAVGCIPLCPQELSLPNLGCPNPR 149
    |||||||||||||||||||     :     .:|||||||||||||||||||

151 LVKVTGQCCEEWVCDEDSIKDPMEDQDGLLGKGLGFDASEVELTRNNELI 200
    ||||.|||||||||||||||:       |:      |:||||||||||||.
150 LVKVSGQCCEEWVCDEDSIKDSLDDQDDL....LGLDASEVELTRNNELI 195

201 AVGKGSSLKRLPVFGMEPRILYNPL...QGQKCIVQTTSWSQCSKTCGTGI 248
    |:||||||||||||||| ||||||||   :|||||||||||||||.|||||
196 AIGKGSSLKRLPVFGTEPRVLFNPLHAHGQKCIVQTTSWSQCSKSCGTGI 245

249 STRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVR 298
    ||||||||||||||||||||||||||||||||||||||||||||||||||
246 STRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVR 295

299 FTYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFPCEDGETFSKNV 348
    ||||||.||||||||||||||||||||| |||||||||.|||||.|||||
296 FTYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNV 345

349 MMIQSSKCNYNCPHANEAAFPFYRLFQ 375
    |||||.||||||||.||||:.|.:.||.
346 MMIQSCKCNYNCPHPNEASFRLYSLFN 372
```

```
                    c  c  c
ATGAGCTCCCGGAATCGTCAGGGAGCTGGCCTTAGTGGTCACCCTTCTCCACTTGACCAGG
M  S  S  R  I  R  R  L  A  L  V  V  T  L  L  H  L  T  R
                              *G
 c  c                         *A
GTGGGGCTCTCCACCTGCCCCGCTGACTGCCACTGCCACTGCCCCCTGGAGGCCCCAAGTGGCCG
L  S  T  C  P  A  X  C  H  C  P  L  E  A  P  K  C  A
   A  L
                           c
CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGTAAGGTCTGCGCCAAGCAGCTC
P  G  V  G  L  V  R  D  G  C  G  C  K  V  C  A  K  Q  L
               c
AACGAGGACTGCAGAAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC
N  E  D  C  R  K  T  Q  P  C  D  H  T  K  G  L  E  C  N  F
         *S
GGCGCCCAGCTCCACCGCCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT
G  A  S  S  T  A  L  K  G  I  C  R  A  Q  S  E  G  R  P  C
GAATATAACTCCAGAATCTACCAAAACGGGAAAGTTTCCAGCCCAACTGTAAACATCAG
E  Y  N  S  R  I  Y  Q  N  G  E  S  F  Q  P  N  C  K  H  Q
                      T
TGCACATGTATTGATGGGCGCGGGGCTGCATTCCTCTGTGTCCCAAGAACTATCT
C  T  C  I  R  R  R  A  C  I  P  L  C  P  Q  E  L  S
         A  G      *A  *V  G
CTCCCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAG
L  P  N  L  G  C  P  N  P  R  L  V  K  V  T  G  Q  C  C  E
MATCH WITH FIG.1B
```

FIG.1A

MATCH WITH FIG.1A

GAGTGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTT
E W V C D E D S I K D P M E D Q D G L L

GGCAAGGNGCTGGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATT
G K E L G F D A S E V E L T R N N E L I

GCAGTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATC
A V G K G S S L K R L P V F G M E P R I

CTATACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGC
L Y N P L Q G Q K C I V Q T T S W S Q C

TCAAAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGC
S K T C G T G I S T R V T N D N P E C R

CTTGTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGC
L V K E T R I C E V R P C G Q P V Y S S

CTGAAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCGAACCAGTCAGGTTTACT
L K K G K C S K T K K S P E P V R F T
MATCH WITH FIG.1C

FIG.1B

MATCH WITH FIG.1B

```
TACGCTGGATGTGTTGAGTGTGAAGAAATACCGGCCAAGTACTGCGGTTCCTGCGTGGAC
Y  A  G  C  L  S  V  K  K  Y  R  P  K  Y  C  G  S  C  V  D
```

```
GGCCGATGCTGCACGCCCCCAGTGACCAGGACTGTGAAGATGCGGTTCCTCTGCGAAGAT
G  R  C  C  T  P  Q  L  T  R  T  V  K  M  R  F  F  C  E  D
                                             R
```

```
GGGGAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTCCAAATGCAACTACAACTGC
G  E  T  F  S  K  N  V  M  M  I  Q  S  S  K  C  N  Y  N  C
                                       C
```

```
CCGCATGCCAATGAAGAGGCGGTTCCCTTCTACAGGCTGTTCCAATGACATTCACAAA
P  H  A  N  E  A  A  F  P  F  Y  R  L  F   AND  I  H  K
                                          F  R   D  *
TTTAGGGACTAA
```

FIG.1C

```
1   MSSRIVRELALAVTLHLITRVGLSTCPADCHCPLEAPKCAPGVGLVRDGG   50
    |||:::::|:::|||||||:::||||||::|||||||||||||||||||
1   MSSSTFRTLAVAVTLLHLTRLALSTCPAACHCPLEAPKCCAPGVGLVRDGC   50

51  GCCKVCAKQLNEDCRKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPC   100
    |||||||||||||:||||||||||||||||||||||||||||||||||||
51  GCCKVCAKQLNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPC   100

101 EYNSRIYQNGESFQPNCKHQCTCIGWRRGACIPLCPQELSLPNLGCPNPR   150
```

MATCH WITH FIG.2B

FIG.2A

FIG. IA

```
ATGAGCTCCCGAATCGTCAGGGAGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG
 M  S  R  I  V  R  E  L  A  L  V  V  T  L  L  H  L  T  R

GTGGGGCTCTCCACCTGCCCCGCTGACTGCCACCCCCTGGAGGCGCCAAGTGCGCG
 V  G  L  S  T  C  P  A  D  C  H  C  P  L  E  A  P  K  C  A

CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGGTGTTGTAAGGTCTGCGCAAGCAGCTC
 P  G  V  G  L  V  R  D  G  C  G  C  C  K  V  C  A  K  Q  L

AACGAGGACTGCAGAAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC
 N  E  D  C  R  K  T  Q  P  C  D  H  T  K  G  L  E  C  N  F

GGCGCCAGCTCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGGCAGACCCTGT
 G  A  S  S  T  A  L  K  G  I  C  R  A  Q  S  E  G  R  P  C

GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCAACTGTAAACATCAG
 E  Y  N  S  R  I  Y  Q  N  G  E  S  F  Q  P  N  C  K  H  Q

TGCACATGTATTGGATGGCGCGGGGGGGCTTGCATTCCTCTGTGTCCCAGAGAACTATCT
 C  T  C  I  G  W  R  G  C  I  P  L  C  P  Q  E  L  S

CTCCCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAGTTACCGGCAGTGCTGCGAG
 L  P  N  L  G  C  P  N  P  R  L  V  K  V  T  G  Q  C  C  E
```

MATCH WITH FIG. IB

FIG. IB

```
        .         .         .         .         .         .
GAGTGGGGTCTGTTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGGCCTCCTT
E   W   V   C   D   E   D   S   I   K   D   P   M   E   D   Q   D   G   L   L

        .         .         .         .         .         .
GGCAAGGGGCTGGGGGATTCGATGCCTCCGAGGTGGTGGAGTTGACGAGAAACAATGAATTGATT
G   K   G   L   G   F   D   A   S   E   V   E   L   T   R   N   N   E   L   I

        .         .         .         .         .         .
GCAGTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGGCATC
A   V   G   K   G   S   S   L   K   R   L   P   V   F   G   M   E   P   R   I

        .         .         .         .         .         .
CTATACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGC
L   Y   N   P   L   Q   G   Q   K   C   I   V   Q   T   S   W   S   Q   C

        .         .         .         .         .         .
TCAAAGACCTGTGGAACTGGTATCTCCACGAGTTACCAATGACAACCCTGAGTGCCGC
S   K   T   C   G   I   S   T   R   V   T   N   D   N   P   E   C   R

        .         .         .         .         .         .
CTTGTGAAAGAAACCCGGATTTGTGTGAGGTGGCCTTGTTGGACAGCCAGTGTACAGCAGC
L   V   K   E   T   R   I   C   E   V   R   P   C   G   Q   P   V   Y   S   S

        .         .         .         .         .
CTGAAAAAGGGCAAGAAATGCAGCAAGAAATCCCCGAACCAGTCAGGTTTACT
L   K   G   K   K   C   S   K   K   S   P   E   V   R   F   T
```

FIG. IC

```
TACGCTGGATGTTTTGAGTGTGAAGAATACCGGCCCAAGTACTGCGGGTTCCTGCGTGGAC
 Y  A  G  C  L  S  V  K  K  Y  R  P  K  Y  C  G  S  C  V  D

GGCCGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGAATGCGGGTTCCCCTGCGAAGAT
 G  R  C  C  T  P  Q  L  T  R  T  V  K  M  R  F  P  C  E  D

GGGGAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTCCAAATGCAACTACAACTGC
 G  E  T  F  S  K  N  V  M  M  I  Q  S  S  K  C  N  Y  N  C

CCGCATGCCAATGAAGCAGCGGTTTCCCTTCTACAGGCTGTTCCAATGA
 P  H  A  N  E  A  A  F  F  Y  R  L  F  Q  *
```

FIG. 2A

```
1 MSSRIVRELALVVTLLHLTRVGLSTCPADCHCPLEAPKCAPGVGLVRDGC   50
  |||...|..||:.||:||||||.:||||||.|||||||||||||||||
1 MSSSTFRTLAVAVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGC   50

51 GCCKVCAKQLNEDCRKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPC  100
   |||||||||||||||.|||.|||||||||||||||||||||||||||||
51 GCCKVCAKQLNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPC  100

101 EYNSRIYQNGESFQPNCKHQCTCIGWRRGACIPLCPQELSLPNLGCPNPR  150
```

FIG. 2B

```
101 EYNSRIYQNGESFQPNCKHQCTCID.GAVGCIPLCPQELSLPNLGCPNPR 149
    |||||||||||||||||||||||:    .:|||||||||||||||||| |
151 LVKVTGQCCEEWVCDEDSIKDPMEDQDGLLGKGLGFDASEVELTRNNELI 200
    ||||·|||||||||||||||||·||:|        ||·||||||||||||||
150 LVKVSGQCCEEWVCDEDSIKDSLDDQDDL....,.LGLDASEVELTRNNELI 195

201 AVGKGSSLKRLPVFGMEPRILYNPL...QGQKCIVQTTSWSQCSKTCGTGI 248
    |:||||||||||||||·||||·|:|||    :||||||||||||||||·|·||||
196 AIGKGSSLKRLPVFGTEPRVLFNPLHAHGQKCIVQTTSWSQCSKSCGTGI 245

249 STRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVR 298
    |||||||||||||||||||||||||||||||||||||||||||||||||||
246 STRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVR 295

299 FTYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFPCEDGETFSKNV 348
    ||||||·||||||||||||||||||||||·||||||||||·||||||·||||
296 FTYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNV 345

349 MMIQSSKCNYNCPHANEAAFPFYRLFQ 375
    ||||:·||||||||||||:·:||·|·||·
346 MMIQSCKCNYNCPHPNEASFRLYSLFN 372
```

FIG. 3

```
  1 MSSRIVRELALVVTLLLHL.TRVGLS.TCPADCHCPLE.APKCAPGVGLVR  47
    | ..:..||.||||.......:|||.::||..|.|:||.|.|:||...||:||
  1 MLASVAGPISLALVLLALCTRPATGQDCSAQCQCAAEAAPHCPAGVSLVL   50

 48 DGGCGCKVCAKQLNEDCRKTQPCDHTKGLECNFGASSTALKGICRAQSEG  97
    ||||||.||||||:..||.:.||||.|||.|.:|....:|||.||:|..|
 51 DGGCGCCRVCAKQLGELCTERDPCDPHKGLFCDFGSPANRKIGVCTAK.DG  99

 98 RPCEYNSRIYQNGESFQPNCKHQCTCIGWRRGACIPLCPQELSLPNLGCP 147
    .||..:.|:|..|||||..:||:|||||:..:.||.|||.:.:||...||
100 APCVFGGSVYRSGESFQSSCKYQCTCLD.GAVGCVPLCSMDVRLPSPDCP 148

148 NPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLGKGLGFDASEVELTRNN 197
    .||:|:|.|.||:|||||:.|.:.|.:.:.:.||      |:    :.::
149 FPRRVKLPGKCCKEWVCDEPKDRTAV...:..:..... GPALAAYRLEDT...: 186

198 ELIAVGKGSSLKRLPVFGMEPRILYNPLQGQKCIVQTTSWSQCSKTCGTG 247
    .........:  ........FGPDPTMM....  || .::  .||||.||||:||
187 .........:  ........FGPDPTMM....RANCLVQTTEWSACSKTCGMG 215

248 ISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPV 297
    |||||||||..|||.|:.||.|.|||||.:.||||||||||:.|.|:.||
216 ISTRVTNDNTFCRLEKQSRLCMVRPCEADLEENIKKGKKCIRTPKIAKPV 265

298 RFTYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFPCEDGETFSKN 347
    :|..:.|||||.|:.|.||.|.|||||||:|.||...:.|.||||.|.||
266 KFELSGCTSVKTYRAKFCGVCTDGRCCTPHRTTTLPVEFKCPDGEIMKKN 315

348 VMMIQSSKCNYNCPHANE..AAFPFYRLFQ 375
    :.|:..:.|.|||||...:..:|:..|.::
316 MMFIKTCACHYNCPGDNDIFESLYYRKMYG 345
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